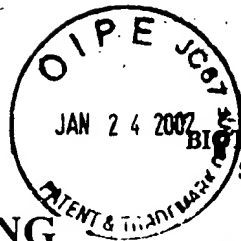
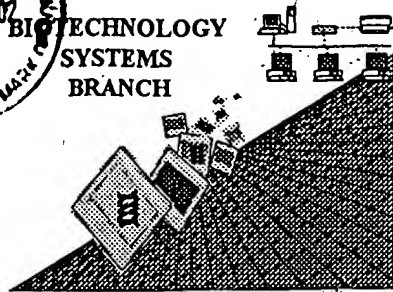


0510  
1217



BIO TECHNOLOGY  
SYSTEMS  
BRANCH



## RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/772,134A  
Source: O I P E  
Date Processed by STIC: 12/18/01

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE: SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by the treatment given to all mail coming via the Brentwood Mail Facility.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom, including:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission

User Manual - ePAVE)

2. U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202

3. Hand Carry directly to:

U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name,  
1911 South Clark Street, Crystal Mall One, Sequence Information, Arlington, VA 22202

Or

U.S. Patent and Trademark Office, 2011 South Clark Place, Customer Window, Box Sequence, Crystal Plaza Two,  
Lobby, Room 1B03, Arlington, Virginia 22202

4. Federal Express Delivery, 2011 South Clark Street, Crystal Plaza 2, Room 1B03-Mailroom, Box Sequence,  
Arlington, VA 22202

## Raw Sequence Listing Error Summary .

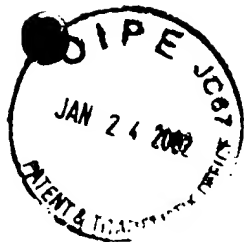
### ERROR DETECTED

### SUGGESTED CORRECTION

SERIAL NUMBER: 091772,134A

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1        Wrapped Nucleics  
    Wrapped Aminos     The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
  
- 2        Invalid Line Length     The rules require that a line not exceed 72 characters in length. This includes white spaces.
  
- 3        Misaligned Amino  
    Numbering     The numbering under each 5<sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
  
- 4        Non-ASCII     The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
  
- 5        Variable Length     Sequence(s)        contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
  
- 6        PatentIn 2.0  
    "bug"     A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s)       . Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
  
- 7        Skipped Sequences  
    (OLD RULES)     Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence:  
                               (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               (i)         SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)  
                               (xi)        SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)  
                               This sequence is intentionally skipped  
  
                               Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
  
- 8        Skipped Sequences  
    (NEW RULES)     Sequence(s)        missing. If intentional, please insert the following lines for each skipped sequence.  
                               <210> sequence id number  
                               <400> sequence id number  
                               000
  
- 9 ✓        Use of n's or Xaa's  
    (NEW RULES)     Use of n's and/or Xaa's have been detected in the Sequence Listing.  
                               Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.  
                               In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
  
- 10        Invalid <213>  
    Response     Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
  
- 11        Use of <220>     Sequence(s)        missing the <220> "Feature" and associated numeric identifiers and responses.  
                               Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.  
                               (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
  
- 12        PatentIn 2.0  
    "bug"     Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.



O I P E

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/09/772,134A

DATE: 12/18/2001  
 TIME: 10:27:06

Input Set : A:\seq list 1268-4-2.ST25.txt  
 Output Set: N:\CRF3\12182001\I772134A.raw

**Does Not Comply  
 Corrected Diskette Needed**

*Errors on pp. 3+4*

```

3 <110> APPLICANT: Lightfoot, David
4      Meksem, Khalid
6 <120> TITLE OF INVENTION: ISOLATED POLYNUCLEOTIDES AND POLYPEPTIDES RELATING TO LOCI
7      UNDERLYING RESISTANCE TO SOYBEAN CYST NEMATODE AND SOYBEAN
8      SUDDEN DEATH SYNDROME AND METHODS EMPLOYING SAME
10 <130> FILE REFERENCE: 1268/4/2
:--> 12 <140> CURRENT APPLICATION NUMBER: US/09/772,134A
:--> 12 <141> CURRENT FILING DATE: 2001-12-18
12 <150> PRIOR APPLICATION NUMBER: 60/178,811
13 <151> PRIOR FILING DATE: 2000-01-28
15 <160> NUMBER OF SEQ ID NOS: 122
17 <170> SOFTWARE: PatentIn version 3.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 87
21 <212> TYPE: DNA
22 <213> ORGANISM: soybean
24 <400> SEQUENCE: 1
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27 tgggtttctg ataaccgtgg tcgttaa                                          87
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31 <211> LENGTH: 92
32 <212> TYPE: DNA
33 <213> ORGANISM: soybean
35 <400> SEQUENCE: 2
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38 agatttgggt ttcagataac cgtggctcgt aa                                    92
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42 <211> LENGTH: 113
43 <212> TYPE: DNA
44 <213> ORGANISM: soybean
46 <400> SEQUENCE: 3
47 gaattcctaa tatacgagtg aatattattg taatgcttgt aaaaaaacat gataaaatgc      60
49 aaaaatttgg ggtgaatttt tacgacatta gtgaaaaaaa catatccctt taa          113
52 <210> SEQ ID NO: 4
53 <211> LENGTH: 135
54 <212> TYPE: DNA
55 <213> ORGANISM: soybean
57 <400> SEQUENCE: 4
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60 tttgaaaaaa tgtactagat atatcatggt tttttacaag cattacaata atatcactc      120
62 gtatattagg aattc                                                        135
65 <210> SEQ ID NO: 5
66 <211> LENGTH: 116
67 <212> TYPE: DNA
68 <213> ORGANISM: soybean
70 <400> SEQUENCE: 5
71 gaattccggt tatctcagac aacttttgggt tggtttgggt atagtaaaga cacgattatc      60

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*end*  
 ↓

The type of errors shown exist throughout the Sequence Listing. Please check subsequent sequences for similar errors.

## RAW SEQUENCE LISTING

DATE: 12/18/2001

PATENT APPLICATION: US/09/772,134A

TIME: 10:27:06

Input Set : A:\seq list 1268-4-2.ST25.txt

Output Set: N:\CRF3\12182001\I772134A.raw

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73 caggctttga gaggcataga aataattttt ttatataaaa aaaaaagtct ctttaa      116
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77 <211> LENGTH: 113
78 <212> TYPE: DNA
79 <213> ORGANISM: soybean
81 <400> SEQUENCE: 6
82 gaatttcggt tatctcagac aacttttggt tggtttggt atagtaaaga cacgattatc      60
84 caggctttga gaggcataga aataattttt ttatataaaa aaaagtctct tta      113
87 <210> SEQ ID NO: 7
88 <211> LENGTH: 409
89 <212> TYPE: DNA
90 <213> ORGANISM: soybean - Forrest
92 <400> SEQUENCE: 7
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95 gcaaacgata atataattat aagaaaaaga cacactttga gggcattttt gacttgagag      120
97 aactcaggta tcaatctaaa agcaacgctg ttcaccttga gctgaaacac ctggaggaga      180
99 aagcaaagca aaccaaagcg gagagagaaa taaagaacgg aaacagagag agagagagga      240
101 aggaccttgt tcaaagcaac ggggacaact ttagagccct ggcgcgcgtg ggggtcaata      300
103 agcgtaacct ggctgaggag agcctcggcg tcgtccttgc tgaagcagaa gaggaagagc      360
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111 <213> ORGANISM: soybean
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118 ttgacttgag agaactcagg tatcaatcta aaagcaacgc tgttcacctt gagctgaaac      180
120 acctggagga gaaagcaaa caaaccaaac gcgagagaga aataaagaac ggaaacagag      240
122 agagaggaag gaccttggtc aaagcaacgg ggacaacttt agagccctgg cgcgcgtggg      300
124 ggtcaataag cgtaacctgg ctgaggagag cctcggcgcc gtccttgctg aagcagaaga      360
126 ggaagagccc gagaccaaga gaaactcctc ggaagcaacg ggaattggta cgcagtc      417
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130 <211> LENGTH: 165
131 <212> TYPE: DNA
132 <213> ORGANISM: soybean
134 <400> SEQUENCE: 9
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137 actttttttt attgaaaaaa tcgacccaag ttgaaacaca tgtttgagaa ttgttttggt      120
139 catccaacgt tttcttgta caatcagctg tgagagggga attgg      165
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143 <211> LENGTH: 164
144 <212> TYPE: DNA
145 <213> ORGANISM: soybean
147 <400> SEQUENCE: 10
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150 ctttttttta ttgaaaaaat cgacccaagt tgaaacacat gtttgagaat tgttttggtg      120
152 atccaacggt tttcttgta aatcagctgt gagaggggaa ttgg      164
155 <210> SEQ ID NO: 11

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## RAW SEQUENCE LISTING

DATE: 12/18/2001

PATENT APPLICATION: US/09/772,134A

TIME: 10:27:06

Input Set : A:\seq list 1268-4-2.ST25.txt

Output Set: N:\CRF3\12182001\I772134A.raw

156 <211> LENGTH: 114  
 157 <212> TYPE: DNA  
 158 <213> ORGANISM: soybean  
 160 <400> SEQUENCE: 11  
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 163 ggaactgcta ttcttacttc taaatttttt attgacatcc aaagtgtgct ttaa 114  
 166 <210> SEQ ID NO: 12  
 167 <211> LENGTH: 114  
 168 <212> TYPE: DNA  
 169 <213> ORGANISM: soybean  
 171 <400> SEQUENCE: 12  
 172 gaattcccag ccagatttgt atcaaacatg tattgtccac aaaatgttca agcatcttag 60  
 174 ggaactgcta ttcttacttc taaatttttt attgacatcc aaagtgtgct ttaa 114  
 177 <210> SEQ ID NO: 13  
 178 <211> LENGTH: 3106  
 179 <212> TYPE: DNA  
 180 <213> ORGANISM: soybean  
 182 <220> FEATURE:  
 183 <221> NAME/KEY: misc\_feature  
 184 <223> OTHER INFORMATION: n is an undetermined nucleotide (dATP, dCTP, dGTP, or dTTP)  
 187 <400> SEQUENCE: 13  
 188 aatgggagga gtgggaaaga cagtggctat ggagcttggt cggagggttg ggttggaatc 60  
 190 aagtgtgctc agggacaggt tattgtgatc cagcttcctt ggaagggttt gaggggtcga 120  
 192 atcaccgaca aaattggcca acttcaaggc ctcaggaagc ttagtcttca tgataaccaa 180  
 194 attggtgggt caatcccttc aactttggga cttcttccca accttagagg ggttcagtta 240  
 196 ttcaacaata ggcttacagg ttccatacct ctttcttttag gtttctgcct ttgcttcaag 300  
 198 tctcttgacc tcagcaacaa cttgtctaca ggagcaatcc cttatagtct tgctaattcc 360  
 200 actaagcttt attggcttaa cttgagtttc aaactcctct ctggctcctt accagctagc 420  
 202 ctaactcact cattttctct cacttttctt tctcttcaaa ataacaatct ttctggctcc 480  
 204 cttcctaact cttgggggtg gaattccaag aatggcttct ttaggcttca aaatttgatc 540  
 206 ctatgcata actttttcac tgggtgacgt cctgcttctt tgggtagctt aagagagctc 600  
 208 aatgagattt cccttagtca taataagttt agtggagcta taccaaatga aataggaacc 660  
 210 ctttctagga ttaagacact tgacatttct aataatgcct tgaatgggaa cttgcctgct 720  
 212 accctctcta atttatectc acttacactg ctgaatgcag agaacaacct ccttgacaat 780  
 214 caaatccctc aaagtttagg tagattgcgt aatctttctg ttctgatttt gagtagaaac 840  
 216 caatttagtg gacatattcc ttcaagcatt gcaaacattt cctcgcttag gcagcttgat 900  
 218 ttgtcactga ataatttcag tggagaaatt ccagttctct ttgacagtca gcgcagtcta 960  
 220 aatctcttca atgtttccta caatagcctc tcaggttctg tccccctct gcttgccaag 1020  
 222 aaatttaact caagctcatt tgtgggaaat attcaactat gtgggtacag cccttcaacc 1080  
 224 ccatgtcttt cccaagctcc atcacaagga gtcattgcc cacctcctga agtgtcaaaa 1140  
 226 catcaccatc ataggaagct aagcaccaaa gacataattc tcatagtagc aggagttctc 1200  
 228 ctcgtagtcc tgattatact ttgttggtgc ctgcttttct gcctgatcag aaagagatca 1260  
 230 acatctagga cgggaacggc caagccaccc gagggtagag cggccactat gaggacagaa 1320  
 232 aaaggagtcc ctccagttgc tgggtggtgat gttgaagcag gtggggaggc tggagggaaa 1380  
 234 ctagtccatt ttgatggacc aatggctttt acagctgatg atctcttggt tgoaacagct 1440  
 236 gagatcatgg gaaagagcac ctatggaact gtttataagg ctattttgga ggatgggaagt 1500  
 238 caagttgcag taaagagatt gagggaaaag atcactaaaag gtcatagaga atttgaatca 1560  
 240 gaagtcagtg ttctagggaa aattagacac cccaatgttt tggctctgag ggcctattac 1620  
 242 ttgggaccca aaggggaaaa gcttctgggt tttgatacat gtctaaagga agtcttgctt 1680

*must give location of n in <223>  
 see error summary sheet item 9*

## RAW SEQUENCE LISTING

DATE: 12/18/2001

PATENT APPLICATION: US/09/772,134A

TIME: 10:27:06

Input Set : A:\seq list 1268-4-2.ST25.txt

Output Set: N:\CRF3\12182001\I772134A.raw

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246 tttaattata atttgaggtt ttaccttagt aatctgtata attctaactg gagaacagta 1800
v--> 248 caaacaaaaa cacctaagga acaacacctt anctttaata taccatatca ataaagtga 1860
250 atattttctt ggtcatcttg atgcaggggg aactgaacat tcattattgg ccacaagatt 1920
252 aaaatagccc aagccttggc cggggcttgt ttgccttcac tcccaggaga acatcataca 1980
v--> 254 tgggacctcn catccagcaa tgtgtggcct gatgaaaaac aaatgctaaa attcagattt 2040
256 tggctctttt cgggttgatg tcaactgctg ctaattccaa cgtgatagct acagctggag 2100
258 cattggatac cgggcacctg agctctcaaa gctcaagaaa gcaaacta aaactgatat 2160
260 ctacagtctt ggtgttatct tgttagaact cctaacgagg aaatcacctg ggggtgtctat 2220
262 gaatggacta gatttgccct agtgggttgc ctacagtggt aaagaggagt ggacaaatga 2280
264 ggtttttgat gcagacttga tgagagatgc atccacagtt ggcgacgagt tgctaaacac 2340
266 gttgaagctc gctttgcact gtgttgatcc ttctccatca gcacgaccag aagttcatca 2400
268 agttctccag cagctgaaga gattagacca gagagatcag tcacagccag tcccggggac 2460
270 gatatcgtat agcacaatt ttgcattgat tttttgtgc caaatgtagt aggcctacta 2520
272 tatatatgtt ctatgattct ttcattotta tattattttt gcctgtttga atgcttgaat 2580
274 ttgtacatac tcatactaca ataagggtga gttctggtta attttacctc tacctcaaag 2640
276 ctgggggtga attctgtttc ctccaaggca cataatagtt gaaaatagtt ctcaggagca 2700
278 ttcattgttt attctgcaag attctctttc acggtgcta tcttctatgc atgccctgcc 2760
280 cataaatgca ttatgaagaa ttgtaacggc tgtgtttttg gacttcttca aaaagtttat 2820
282 gttattgcca ggtgtatata tcaacatgtt ttaaagattt tcaaacaatc aggttttaga 2880
284 tgtgggtttg catgcatgag attggactag tgcgcttgat gtagtataaa atataaatg 2940
286 tccaatcaag caccctctac atgtccaaat aatgggcctt atgaaactta attttttaat 3000
i--> 288 tacaactac agtaatcttt ttgaataaag atttacaaat tacaacngac atgtgaagen 3060
i--> 290 gcactctttna ttgncaatct ttcaagttac tctattattt tctgcn 3106
293 <210> SEQ ID NO: 14
294 <211> LENGTH: 830
295 <212> TYPE: PRT
296 <213> ORGANISM: soybean
298 <220> FEATURE:
299 <221> NAME/KEY: misc_feature
300 <223> OTHER INFORMATION: X is any amino acid
303 <400> SEQUENCE: 14
305 Asn Gly Arg Ser Gly Lys Asp Ser Gly Tyr Gly Ala Cys Ser Gly Gly
306 1 5 10 15
308 Trp Val Gly Ile Lys Cys Ala Gln Gly Gln Val Ile Val Ile Gln Leu
309 20 25 30
311 Pro Trp Lys Gly Leu Arg Gly Arg Ile Thr Asp Lys Ile Gly Gln Leu
312 35 40 45
314 Gln Gly Leu Arg Lys Leu Ser Leu His Asp Asn Gln Ile Gly Gly Ser
315 50 55 60
317 Ile Pro Ser Thr Leu Gly Leu Leu Pro Asn Leu Arg Gly Val Gln Leu
318 65 70 75 80
320 Phe Asn Asn Arg Leu Thr Gly Ser Ile Pro Leu Ser Leu Gly Phe Cys
321 85 90 95
323 Pro Leu Leu Gln Ser Leu Asp Leu Ser Asn Asn Leu Leu Thr Gly Ala
324 100 105 110
326 Ile Pro Tyr Ser Leu Ala Asn Ser Thr Lys Leu Tyr Trp Leu Asn Leu
327 115 120 125
329 Ser Phe Asn Ser Phe Ser Gly Pro Leu Pro Ala Ser Leu Thr His Ser

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*must give location of X in 2227, see error summary sheet, Term 9*

## RAW SEQUENCE LISTING

DATE: 12/18/2001

PATENT APPLICATION: US/09/772,134A

TIME: 10:27:06

Input Set : A:\seq list 1268-4-2.ST25.txt

Output Set: N:\CRF3\12182001\I772134A.raw

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332 Phe Ser Leu Thr Phe Leu Ser Leu Gln Asn Asn Asn Leu Ser Gly Ser
333 145      150      155      160
335 Leu Pro Asn Ser Trp Gly Gly Asn Ser Lys Asn Gly Phe Phe Arg Leu
336      165      170      175
338 Gln Asn Leu Ile Leu Asp His Asn Phe Thr Gly Asp Val Pro Ala
339      180      185      190
341 Ser Leu Gly Ser Leu Arg Glu Leu Asn Glu Ile Ser Leu Ser His Asn
342      195      200      205
344 Lys Phe Ser Gly Ala Ile Pro Asn Glu Ile Gly Thr Leu Ser Arg Leu
345      210      215      220
347 Lys Thr Leu Asp Ile Ser Asn Asn Ala Leu Asn Gly Asn Leu Pro Ala
348 225      230      235      240
350 Thr Leu Ser Asn Leu Ser Ser Leu Thr Leu Leu Asn Ala Glu Asn Asn
351      245      250      255
353 Leu Leu Asp Asn Gln Ile Pro Gln Ser Leu Gly Arg Leu Arg Asn Leu
354      260      265      270
356 Ser Val Leu Ile Leu Ser Arg Asn Gln Phe Ser Gly His Ile Pro Ser
357      275      280      285
359 Ser Ile Ala Asn Ile Ser Ser Leu Arg Gln Leu Asp Leu Ser Leu Asn
360      290      295      300
362 Asn Phe Ser Gly Glu Ile Pro Val Ser Phe Asp Ser Gln Arg Ser Leu
363 305      310      315      320
365 Asn Leu Ser Asn Val Ser Tyr Asn Ser Leu Ser Gly Ser Val Pro Pro
366      325      330      335
368 Leu Leu Ala Lys Lys Phe Asn Ser Ser Ser Phe Val Gly Asn Ile Gln
369      340      345      350
371 Leu Cys Gly Tyr Ser Pro Ser Thr Pro Cys Leu Ser Gln Ala Pro Ser
372      355      360      365
374 Gln Gly Val Ile Ala Pro Pro Glu Val Ser Lys His His His His
375      370      375      380
377 Arg Lys Leu Ser Thr Lys Asp Ile Ile Leu Ile Val Ala Gly Val Leu
378 385      390      395      400
380 Leu Val Val Leu Ile Ile Leu Cys Cys Val Leu Leu Phe Cys Leu Ile
381      405      410      415
383 Arg Lys Arg Ser Thr Ser Lys Ala Gly Asn Gly Gln Ala Thr Glu Gly
384      420      425      430
386 Arg Ala Ala Thr Met Arg Thr Glu Lys Gly Val Pro Pro Val Ala Gly
387      435      440      445
389 Gly Asp Val Glu Ala Gly Gly Glu Ala Gly Gly Lys Leu Val His Phe
390      450      455      460
392 Asp Gly Pro Met Ala Phe Thr Ala Asp Asp Leu Leu Cys Ala Thr Ala
393 465      470      475      480
395 Glu Ile Met Gly Lys Ser Thr Tyr Gly Thr Val Tyr Lys Ala Ile Leu
396      485      490      495
398 Glu Asp Gly Ser Gln Val Ala Val Lys Arg Leu Arg Glu Lys Ile Thr
399      500      505      510
401 Lys Gly His Arg Glu Phe Glu Ser Glu Val Ser Val Leu Gly Lys Ile
402      515      520      525

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## VERIFICATION SUMMARY

DATE: 12/18/2001

PATENT APPLICATION: US/09/772,134A

TIME: 10:27:07

Input Set : A:\seq list 1268-4-2.ST25.txt

Output Set: N:\CRF3\12182001\I772134A.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No  
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date  
L:248 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13  
L:248 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:254 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13  
L:254 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:288 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13  
L:288 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:290 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:13  
L:290 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13  
L:419 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14  
L:419 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:422 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14  
L:422 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:425 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14  
L:425 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:428 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14  
L:428 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:434 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14  
L:434 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:437 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14  
L:437 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:446 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14  
L:446 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:452 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14  
L:452 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:455 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:14  
L:455 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:14  
L:467 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:15  
L:475 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:487 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:493 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:495 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:497 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:15  
L:506 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:16  
L:532 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16  
L:541 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:17  
L:547 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:551 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:553 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:555 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:561 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:563 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:565 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:17  
L:574 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:18



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Input Set : A:\seq list 1268-4-2.ST25.txt

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.:596 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
.:598 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
.:600 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
.:602 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
.:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18  
.:615 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:19  
.:633 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
.:637 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
.:639 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
.:641 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
.:643 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
.:645 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19  
.:683 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20  
.:683 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
.:685 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20  
.:685 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
.:687 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20  
.:687 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
.:689 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:20  
.:689 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:20  
.:717 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21  
.:717 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
.:719 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21  
.:719 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
.:721 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21  
.:721 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
.:723 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21  
.:723 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
.:725 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21  
.:725 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
.:727 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21  
.:727 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21  
.:755 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22  
.:759 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22  
.:761 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22  
.:763 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22  
.:765 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22  
.:767 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22  
.:769 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:22  
.:799 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23  
.:803 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23  
.:805 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23  
.:807 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23  
.:809 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:23  
.:837 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24  
.:839 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24  
.:841 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:24  
.:877 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25  
.:879 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:25

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L:893 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
L:909 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
L:911 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:26  
L:945 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:27  
L:961 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28  
L:963 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28  
L:975 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28  
L:977 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28  
L:979 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28  
L:981 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:28



Met Val Ser Met Phe Ser Leu Ser Phe Lys Trp Pro Gly Phe O/s Leu

1

5

10

15

Phe Val

Numeric Identifier	Definition	Comments and format	Mandatory (M) or optional (O)
<110>	Applicant	Preferably max. of 10 names; one name per line; preferable format: Surname, Other Names and/or Initials.	M
<120>	Title of Invention		M
<130>	File Reference	Personal file reference	M when filed prior to assignment of appl. number.
<140>	Current Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if available.
<141>	Current Filing Date	Specify as: yyyy-mm-dd	M, if available.
<150>	Prior Application Number	Specify as: US 07/999,999 or PCT/US96/99999	M, if applicable. Include priority documents under 35 USC 119 and 120.
<151>	Prior Application Filing Date	Specify as: yyyy-mm-dd	M, if applicable.
<160>	Number of SEQ ID NOs	Count includes total number of SEQ ID NOs	M.
<170>	Software	Name of software used to create the Sequence Listing.	O.
<210>	SEQ ID NO:1	Response shall be an integer representing the SEQ ID NO shown.	M.
<211>	Length	Respond with an integer expressing the number of bases or amino acid residues.	M.

Numeric Identifier	Definition	Comments and format	Mandatory (M) or optional (O)
<212>	Type	Whether presented sequence molecule is DNA, RNA, or PRT (protein). If a nucleotide sequence contains both DNA and RNA fragments, the type shall be "DNA." In addition, the combined DNA/RNA molecule shall be further described in the <220> to <223> feature section.	M.
<213>	Organism	Scientific name, i.e. Genus/ species, Unknown or Artificial Sequence. In addition, the "Unknown" or "Artificial Sequence" organisms shall be further described in the <220> to <223> feature section.	M
<220>	Feature	Leave blank after <220>. <221-223> provide for a description of points of biological significance in the sequence..	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA
<221>	Name/Key	Provide appropriate Identifier for feature, preferably from WIPO Standard ST.25 (1998), Appendix 2, Tables 5 and 6.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence.
<222>	Location	Specify location within sequence; where appropriate state number of first and last bases/ amino acids in feature.	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence.
<223>	Other Information	Other relevant information; four lines maximum	M, under the following conditions: if "n," "Xaa," or a modified or unusual L-amino acid or modified base was used in a sequence; if ORGANISM is "Artificial Sequence" or "Unknown"; if molecule is combined DNA/RNA.
<300>	Publication Information	Leave blank after <300>	O.
<301>	Authors	Preferably max of ten named authors of publication; specify one name per line; preferable format: Surname, Other Names and/or Initials.	O.
<302>	Title		O.
<303>	Journal		O.
<304>	Volume		O.
<305>	Issue		O.
<306>	Pages		O.
<307>	Date	Journal date on which data published; specify as yyyy-mm-dd, MMM-yyyy or Season-yyyy.	O.
<308>	Database Accession Number	Accession number assigned by database including database name.	O.
<309>	Database Entry Date	Date of entry in database; specify as yyyy-mm-dd or MMM-yyyy.	O.
<310>	Patent Document Number	Document number; for patent-type citations only. Specify as, for example, US 07/999,999.	O.
<311>	Patent Filing Date	Document filing date, for patent-type citations only; specify as yyyy-mm-dd.	O.
<312>	Publication Date	Document publication date, for patent-type citations only; specify as yyyy-mm-dd.	O.
<313>	Relevant Residues	FROM (position) TO (position)	O.
<400>	Sequence	SEQ ID NO should follow the numeric identifier and should appear on the line preceding the actual sequence.	M.